

Input file F1h14273new; Duput File F1h14273tra
Sequence length 1743

	M	S	P	E	C	A	R	A	A	
TCCGGACTAGTTCTAGACCGCTGCGGGCCGCCAGCGCCGGGA	ATG	TCC	CCT	GAA	TGC	GCG	GCG	GCA	GCG	9
G D A P L R S L E Q A N R T R F F S										27
GGC GAC GCG CCC TTG CGC AGC CTG GAG CAA GCC AAC CGC ACC CGC TTT CCC TTC TTC TCC										29
D V K G D H R L V L A A V E T T V L V L										87
GAC GTC AAG GGC GAC CAC CGG CTG GTG CTG GCG GTG GAG ACA ACC GTG CTG GTG CTC										49
I F A V S L L G N V C A L V L V GTG CTG GCG CGC CGA CGA										147
ATC TTT GCA GTG TCG CTG CTG GGC AAC GTG TGC TGC GTG CTG GTG CTG GTG										69
R R G A T A C L V L N L F C A D L L F I										207
CGC CGC GGC GCG ACT GCC TGC CTG GTA CTC AAC CTC TTC TGC GCG GAC CTG CTC TTC ATC										89
S A I P L V L A V R W T E A W L L G P V										267
AGC GCT ATC CCT CTG GTG CTG GCC GTG CGC TGG ACT GAG GCC TGG CTG CTG GGC CCC GTT										109
A C H L L F Y V M T L S G S V T I L T L										327
GCC TGC CAC CTG CTC TTC TAC GTG ATG ACC CTG AGC GGC AGC GTC ACC ATC CTC ACG CTG										129
A A V S L E R M V C I V H L Q R G V R G										387
GCC GCG GTC AGC CTG GAG CGC ATG GTG TGC ATC GRG CAC CTG CAG CGC GGC GTG GGG GGT										149
P G R R A R A V L L A L I W G Y S A V A										447
CCT CGG CGG CGG GCG GCA GTG CTG CTG GCG CTC ATC TGG GCC TAT TCG GCG GTC GGC										169
A L P L C V F F R V V P Q R L P G A D Q										507
GCT CTG CCT CTC TGC TGC TTC TTT CGA GTC GTC CCG CAA CGG CTC CCC GGC GAC CAG										189
										567

TD FIG. 1B.

FIG. 1A.

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FROM FIG. 1A.

E	I	S	I	C	T	L	I	W	P	T	I	P	G	E	I	S	W	D	V	209
GAA	ATT	TCG	ATT	TGC	ACA	CTG	ATT	TGG	CCC	ACC	ATT	CCT	GGA	GAG	ATC	TCG	TGG	GAT	GTC	627
S	F	V	T	L	N	F	L	V	P	G	L	V	I	V	I	S	Y	S	K	229
TCT	TTT	GTT	ACT	TTG	AAC	TTC	TTG	GTG	CCA	GGA	CTG	GTC	ATT	GTG	ATC	AGT	TAC	TCC	AAA	687
I	L	Q	I	T	K	A	S	R	K	R	L	T	V	S	L	A	Y	S	E	249
ATT	TTA	CAG	ATC	ACA	AAG	GCA	TCA	AGG	AAG	AGG	CTC	ACC	GTA	AGC	CTG	GCC	TAC	TCG	GAG	747
S	H	Q	I	R	V	S	Q	Q	D	F	R	L	F	R	T	L	F	L	L	269
AGC	CAC	CAG	ATC	CGC	GTG	TCC	CAG	CAG	GAC	TTC	CGG	CTC	TTC	CGC	ACC	CTC	TTC	CTC	CTC	807
M	V	S	F	F	I	M	W	S	P	I	I	I	T	I	L	L	I	L	I	208
ATG	GTC	TCC	TTC	TTC	ATC	ATG	TGG	AGC	CCC	ATC	ATC	ATC	ACC	ATC	CTC	CTC	ATC	CTG	ATC	867
Q	N	F	K	Q	D	L	V	I	W	P	S	L	F	F	W	V	V	A	F	309
CAG	AAC	TTC	AAG	CAA	GAC	CTG	GTC	ATC	TGG	CCG	TCC	CTC	TTC	TTC	TGG	GTG	GTG	GCC	TTC	927

TO FIG. 1C.

FIG. 1B.

FROM FIG. 1B.

T F A N S A L N P I L Y N M T L C R N E 329
 ACA TTT GCT AAT TCA GCC CTA AAC CCC ATC CTC TAC AAC ATG ACA CTG TGC AGG AAT GAG 987
 W K K I F C C F W F P E K G A I L T D T 349
 TGG AAG AAA ATT TTT TGC TGC TTC TGG TTC CCA GAA AAG GGA GCC ATT TTA ACA GAC ACA ACA 1047
 S V K R N D L S I I S G • 362
 TCT GTC AAA AGA AAT GAC TTG TCG ATT ATT TCT GGC TAA 1086

TTTTTCTTTATAGCCGAGTTTCTCACACCTGGCGAGCTGTGGCATGCTTTTAAACAGAGTTCATTTCCAGTACCCTCCA
 TCAGTGCACCCTGCTTTAAGAAAAATGAACCTATGCAAAATAGACATCCACAGCGTCGGTAAATTAAGGGGTGATCACCAA
 GTTTCATAATATTTTCCCTTTATAAAAGGATTTGTTGGCCAGGTGCAGTGGTTCATGCTGTATCCAGCAGTTTGGG
 AGGCTGAGGTGGTGGATCACCTGAGGTCAGGAGTTCGAGACCAACCTGACCACACATGGTGAGACCCCGTCTCTACTA
 AAAATAAAAAAAAATAAGCTGGGAGTGGTGGGCACCTGTATCCTAGCTACTTGGGAGGCTGAACCGAGGAAT
 CTCCTGAACCTGGGAGGCAGAGTTGCAGTGAGCCGAGATCGTGCCATTGCACCTCCAACCGGCAACAAGAGTGAAC
 TCCATCTTAAAAAAAATAAAGATTGTTATGGGTTCCCTTTTAAATGTGAACCTTTTGTAGTGTGTTGTAAATATG
 ATCAAATTAATAAATATTTATTTATGACTGTTTCAGCAAAAAAAAATAAAGGGCGG

RTA01/2057957v1

FIG. 1C.

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Sequence	Description	score	E-value	N
7tm_1	PF00001 7 transmembrane receptor (rhodopsin)	119.9	4.7e-37	1

Parsed for domains:

Sequence	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value	-
7tm_1	1/1	57	321	1	259 []	119.9	4.7e-37	-

Alignments of top-scoring domains:

7tm_1: domain 1 of 1, from 57 to 321: score 119.9, E = 4.7e-37

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      *->GNILVilviirtkklrtptnifi1NLAVADLLf11t1ppwalyy1vg
      GN+ ++++++r ++r +t +++1NL ADLLf + p++ ++ -+
F1h14273, 57  GNVCALVLVAR-RRRRGATACLVLNLF CADLLFISAIPVLAVR-WT 101

      gaadWpfGsa1CK1vta1dvvnmyaSi11Lta1SiDRY1A1vhP1ryrrr
      e W++G++ C+1+ ++++++ + i1+L+a S++R + Iv 1+ +r
F1h14373, 102 --EAWLLGPVACHLLFYMTLSGSVTILTAAVSLERMVCIV-HLQRGVR 148

      rtsprrrAkvvil1vwv1a111s1Pp11fswvktveegngt1nvnevC1i
      +r +v+++1+W +++++1P +f+ v+ ++ ++ ++ +C++
F1h14273, 149 GPGRRARAVLLALIWGYSAAALPLCVFFRVVPQRLPG--ADQEISICTL 196

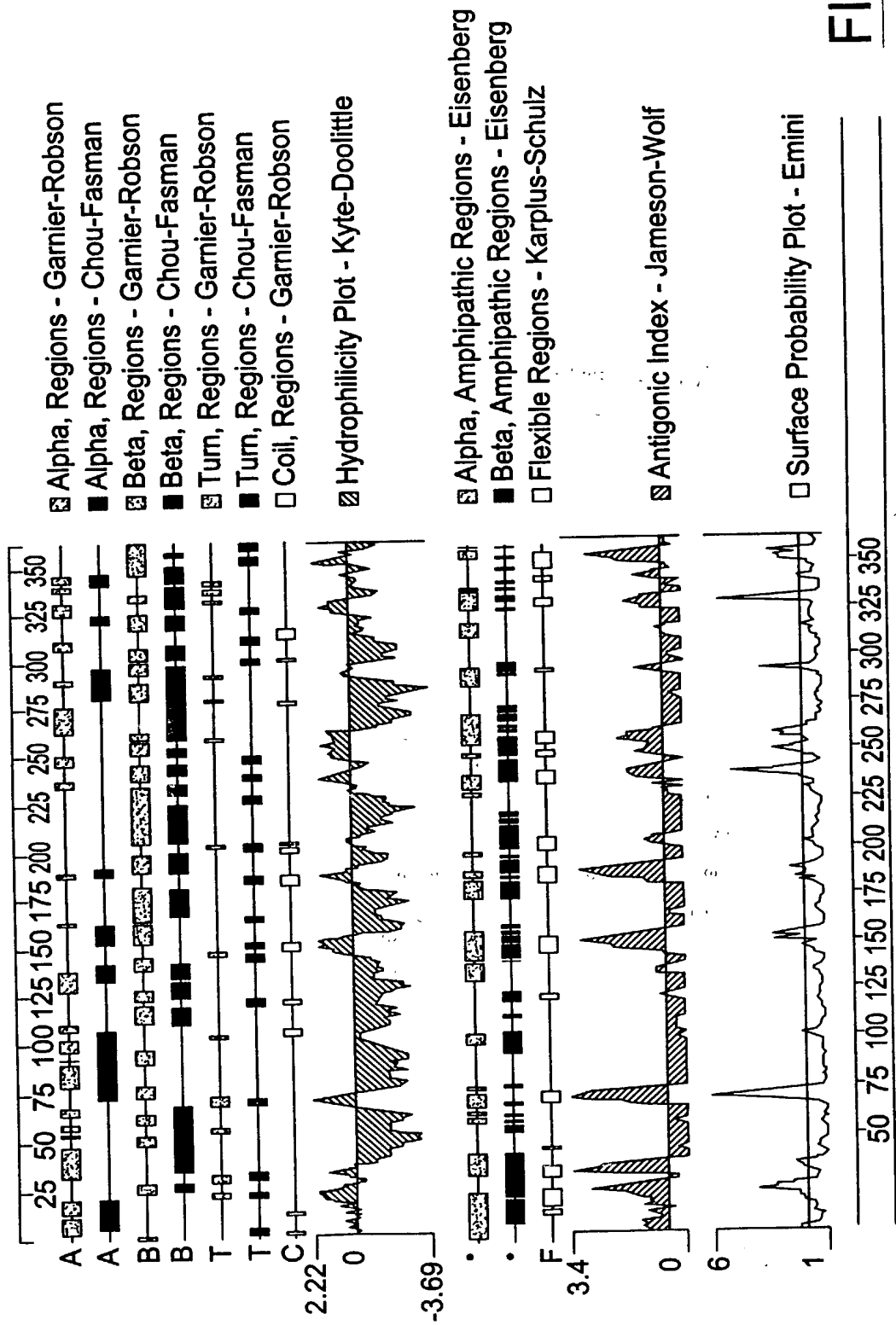
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      +p++++ ++s+ +++ ++ F1+P 1vi++ Y+ I1 + + ++++
F1h14273, 197 IWPTIPG-----EISWDVSFVTNLFVPLVIVISYSKILQITKsrkr 240

      .....:..... kaakt11vvvvvFv1CW1Pyfiv11dt1c
      + + +++++ + ++++ ++ +t1++++v F++ W P i++11 +
F1h14273, 241 1cvslayseehqirvsqqdfRLFRTLFLLMVSFFIMWSPIIITILLILIQ 290

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F1h14273, 291 nFK-----QDLVIWPSLFFWVAPTFA NSALNPILY 321

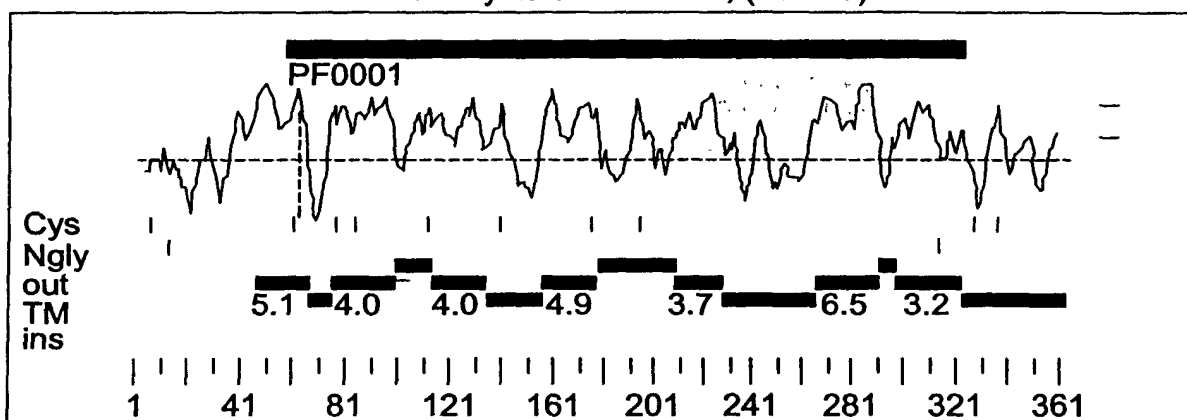
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FIG. 2.



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Analysis of Flh14273, (362 aa)



>F1h14273, 1086 bases, 1825 checksum.
 MSPECARAAQDAPLRSLEQANRTRFPFFSDVKGDHRLVLAAVETTVLVLEFAVSLLGNVC
 ALVLVARRRRRGATAQLVLNLF CADLLFYSAIPLVLAVRWTEAVLLGPVACHLLFYVMTL
 SGSVTILTLAAVSLERMVCIVHLQRCVRGPGRRARAVLLALIWGYSAAALPLCVFFRVV
 PQRLPGADQEISICTLIWPTIPGEISWDVSFVTNFLVPGLVIVISYSKILQITKSRKR
 LTVSLAYSESHQIRVSQQDFRLFRTLFLLMVSFFIMWSPITITILLILIQNFQDLVIWP
 SLFFWVVAFTFANSALNPILYNMTLCRNEWKKIFCCFWFGPEKGAILTDTSVKRNDLSIIS
 G+

FIG. 4.

Prosite Pattern Matches for F1h14273

>PS00001/PDDCC00001/ASN_GLYCOSYLATION N-glycosylation site.

Query: 21 NRTR 24

Query: 322 NMTL 325

>PS00004/PDDCC00004/CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site

Query: 239 KRLT 242

>PS00005/PDDCC00005/PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.

Query: 237 SRK 239

Query: 350 SVK 352

>PS00006/PDDCC00006/CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.

Query: 256 SQQD 259

>PS00008/PDDCC00008/MYRISTYL N-myristoylation site.

Query: 57 GNVCL 62

Query: 72 GATACL 77

Query: 343 GAILTD 348

>PS00009/PDDCC00009/AMIDATION Amidation site.

Query: 150 PCRR 153

>PS00029/PDDCC00029/LEUCINE_ZIPPER Leucine zipper pattern.

Query: 106 LGPVACHLLFYVMTLGSVTL 127

FIG. 5.

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Transmembrane Segments Predicted by MEMSAT

Start	End	Orient	Score
46	66	out->ins	5.1
75	98	ins->out	4.0
113	134	out->ins	4.0
156	177	ins->out	4.9
209	227	out->ins	3.7
266	289	ins->out	6.5
297	321	out->ins	3.2

>F1h14273,

MSPECARAAGDAPLRSLEQANRTRFPFFSDVKGDHRLVLA AVETTVLVLP AVSLLGNVC
 ALVLVARRRRRGATACLVNLFCADLLFISAWPLVLAVRWTEAWLLGPVACHLLFYVMTL
 SGSVTILTAAVSLERMVCIVHLQRGVRGPGRRARAVLLALIWGYSAAALPLCVFFRVV
 PQRLPGADQEISICTLIWPTIPGEISWDVSFVTLNFLVPGLVIVISYSKILQITKASRK
 LTVSLAYSESHQIRVSQQDFRLFRTLFLLMVSFFIMWSPIIITILLILIQNFKQDLVIWP
 SLFFWVVAFTFANSALNPILYNMTCRNEWKKIFCCFWFPEKGAILTDTSVKRNDLSIIS
 G

Transmembrane Segments for Presumed Mature Peptide

Start	End	Orient	Score
14	37	ins->out	4.0
52	73	out->ins	4.0
95	116	ins->out	4.9
148	166	out->ins	3.7
205	228	ins->out	6.5
236	260	out->ins	3.2

>F1h14273, _mature

LVLVARRRRRGATACLVNLFCADLLFISAIPLVLAVRWTEAWLLGPVACHLLPYVMTLS
 GSVTILTAAVSLERMVCIVHLQRGVRGPGRRARAVLLALIWGYSAAALPLCVFFRVVP
 QRLPGADQEISICTLIWPTIPGEISWDVSFVTLNFLVPGLVIVISYSKILQITKASRKRL
 TVSLAYSESHQIRVSQQDFRLFRTLFLLMVSFFIMWSPIIITILLILIQNFKQDLVIWPS
 LFFWVVAFTFANSALNPILYNMTCRNEWKKIPCCFWFPEKGAILTDTSVKRNDLSIISG

FIG. 6.

Input file 14273mj Output File 14273mtra
Sequence length 1560

TTGCCAAGCTCAGCGTAAGCCCTCTTCCACTGCAATCTCACAGAAGGGTTTCATGGAGTGCTTCACACCATCAGTGACCA

CTCCAGACTTGTCGGGCTTTACCCGAATCTTCACAGCGGAGTCGATGACCCCTCTTGACAGCCACGAGCGCGCAGCTC

	M	S	P	E	C	A	Q	T	G	
CGCCATCTTCCCGACGCGTGGGCGGCGCCCGGC	ATG	TCC	CCT	GAG	TGT	GCA	CAG	ACG	ACG	GGC
P G P S H T L D Q V N R T H F P F F S D										
CCT GCT CCC TCG CAC ACC CTG GAC CAA GTC AAT CGC ACC CAC TTC CCT TTC TTC TCG GAT										
V K G D H R L V L S V V E T T V L G L I										
GTC AAG GGC GAC CAC CGG TTG GTG TTG AGC GTC GTG GAG ACC ACC GTT CTG GGA CTC ATC										
F V V S L L L G N V C A L V L V A R R R R										
TTT GTC GTC TCA CTG CTG GGC AAC GTG TGT GCT CTA GTG CTG GTG GCG CGC CGT CGG CGC										
R G A S A S L V L N L F C A D L L L F T S										
CGT GGG GCG TCA GCC AGC CTG GTG CTG AAC CTC TGC TGC GCG GAT TTG CTC TTC ACC AGC										
A I P L V L V V R W T E A W L L G P V V										
GCC ATC CCT CTA GTG CTC GTC GTG CGC TGG ACT GAG GCC TGG CTG TTG GGG CCC GTC GTC										
C H L L F Y V M T M S G S V T I L L A										
TGC CAC CTG CTC TTC TAC ATG ATG ACA ATG AGC AGC AGC GTC ACG ATC CTC ACA CTG GCC										
A V S L E R M V C I V R L R R G L S G P										
GCG GTC AGC CTG GAG CGC ATG GTG TGC ATC GTG CGC CTC CGG CGC GGC TTG AGC GGC CCG										
G R R T Q A A L L A F I W G Y S A L A A										
GGG CGG CGG ACT CAG GCG GCA CTG CTG GCT TTC ATA TGG GGT TAC TCG GCG CTC GCC GCG										

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TD FIG. 7B.

FIG. 7A.

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FROM FIG. 7A.

L P L Y I L L F R V V V P Q R L P G G G D Q E 190
 CTG CCC CTC TAC ATC TTG TTC CGC GTG GTC CCG CAG CAG CGC CTT CCC GGC GGC GAC CAG GAA 627
 I P I C T L L D W P P N R I G E I S W D V F 210
 ATT CCG ATT TGC ACA TTG GAT TGG CCC AAC CGC ATA GGA GAA ATC TCA TGG GAT GTG TTT 630
 F E T L N F L V P G L V I V I S Y S K I 230
 TTT GAG ACT TTG AAC TTC CTG CTG GGA CTG GTC ATT GTG ATC AGT TAC TCC AAA ATT 690
 L Q I T K A S TCG CGG AAG AGG CTT ACG CTG AGC TTG GCA TAC TCT GAG AGC 250
 TTA CAG ATC ACG AAA GCA TCG CCG AAG AGG CTT ACG CTG AGC TTG GCA TAC TCT GAG AGC 750
 H Q I R V S Q Q R Q D Y R L L F R T L F L L M 270
 CAC CAG ATC CGA GTG TCC CAA CAA GAC TAC CGA CTC TTC CGC AGC CTC TTC CTG CTC ATC 810
 V S F F I M W S P I I I I T I L L I L I Q 290
 GTT TCC TTC TTC ATC ATG TGG AGT CCC ATC ATC ATC ACC ATC CTC CTC ATC TTC ATC CAA 870
 N F R Q D L V I W P S L L F F W V A F T 310
 AAC TTC CGG CAG GAC CTG GTC ATC TGG CCA TCC CTT TTC TTC TGG GTG GTG GCC TTC ACG 930
 F A N S A L L N P I L Y N M S L F R N E W 330
 TTT GCC AAC TCT GGC CTA AAC CCC ATA CTG TAC AAC ATG TCG CTG TTC AGG AAC GAA TGG 990
 R K I F C C F F F P E K G A I F T D T S 350
 AGG AAG ATT TTT TGC TGC TGC TGC TTT TTT CCA GAG AAG GGA GCC ATT TTT ACA GAT ACG TCT 1050
 V R R N D L S V I S S • 362
 GTC AGG CGA AAT GAC TTG TCT GTT ATT TCC AGC TAA 1086

CTAGCCTCTGGTGCCAGGTGAACCACGGTGTGCATGTAAAGCGAGTTAACTTCAAGGAAAGCCACCAGTGGCCCTGCG
 TTTAAAAATACCCGACTTCCAACAGCAGGCATCTACGGAGCCAGCAATTAAAGGAATGATCGCTCAGTATAAAAAATATT
 TTTCTTAAAAGAACTTTCTATGGTTCTCTTTTGTGAACCTTTTAAAGTGTTGTGTAATATGATCTAGTTAATAAATT
 TTTATTATAACGTGTTCTCTACAAAAAATAAAAAAATAAAAAA

FIG. 7B.

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Query: 14273m,

Scores for sequence family classification (score includes all domains):

Sequence	Description	Score	E-value	N
7tm_1	PF00001 7 transmembrane receptor (rhodopsin	118.8	1e-35	1

Parsed for domains:

Sequence	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value	-
7tm_1	1/1	57	321	..	1 259 []	118.8	1e-36	

Alignments of top-scoring domains:

7tm_1: domain 1 of 1, from 57 to 321: score 118.8, E = 1e-36

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      *->GNILVilvilrtkk1rtptnifi1NLAvADLLf11tlppwalyylvg
      GN+ +++++tr +tr ++ +1NL ADLLf+ + p++ ++ ++
14273m, 57  GNVCALVLVAR-RRRGASASLVNLFCADLLFTSAIPLVLVVR-WT 101

      gaadWpfGaa1Ck1vta1dvvnmyaSi111Lta1SiDRY1A1vhP1ryrrr
      e W++G+++C+1+ ++++++ + i1+L+a S++R + Iv 1r +
14273m, 102 --EAWLLGPVVCHLLPYVMTMSGSVTILTLAAVSLERMVCIV-RLRRGLS 148

      rtsprra.kvvi1lvv1a111s1Pp11fswvktveagngt1nvvnvtvC1
      rr+++++++W ++1++1P +++++ v + ++g ++ +C+
14273m, 149 GP-GRRTqAALLAFIWGYSALAALPLYILFRVVPQRLPGGD--QEITPCT 195

      idfpeestasvstw1rsyv11st1vgF21P11vilvoYtr11rt1r....
      +d+p++ + ++s+ +++ ++ F1+P 1vi++ Y+ 11 + + +++
14273m, 196 LDWPNRIG-----EISWDVFFETLNFLVPGLVIVISYSKILQITKsrk 239

      ..... kaakt11vvvvvFv1CW1Pyfiv111dt-
      + + + +++++ + +++++ ++ +t1++++v F++ W P i++11 +
14273m, 240 r1t1slayseshqirvsqqdyRLFRTLFLLMVSFFIMWSPIIITILLILI 289

      c.1aiimestCelervlptallvt1wLayvNsc1NP11Y<-*
      ++ + + p +++++ + +++++Ns+1NPi+Y
14273m, 290 QnFR-----QDLVIWPSLFFWVVAFTFANSALNPILY 321

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FIG. 8.

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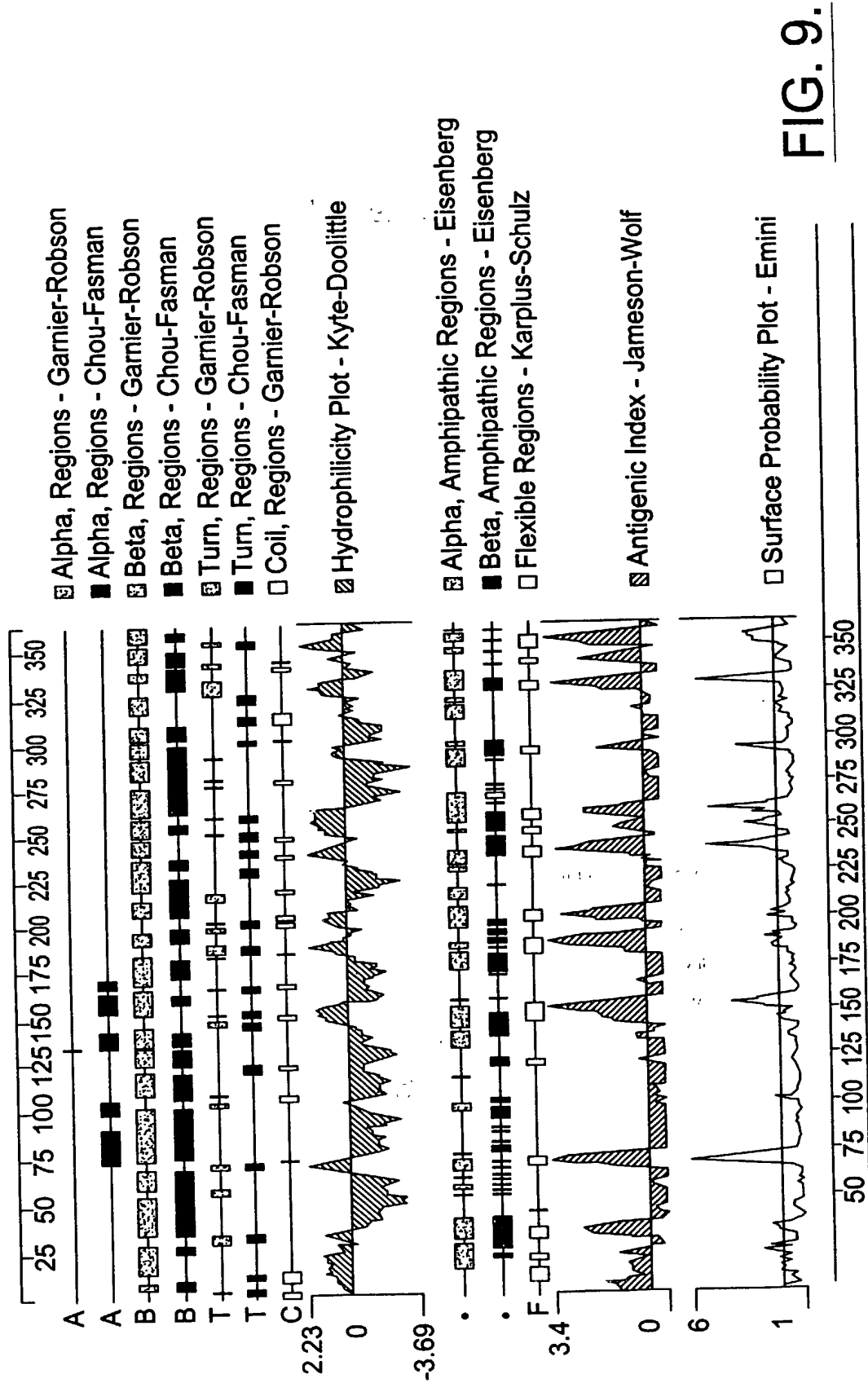
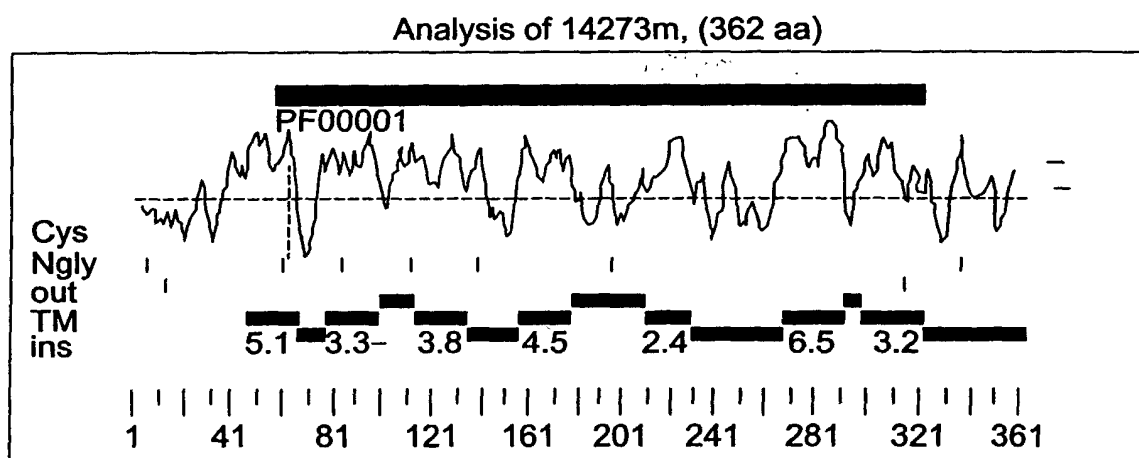


FIG. 9.

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>14273m, 1086 bases, 6943 checksum.
 MSPECAQTGPCPSHTLDQVNRTHFPFFSDVKGDHRLVLSVVETTVLGLIFVVSLLGNVC
 ALVLVARRRRRGASASLVNLF CADLLFTSAIPLVLVVRWTEAWLLGPVVCHLLFVMTM
 SGSVTILTLAAVSLERMVCIVRLRRGLSGPGRRTQAALLAFIWGYSALAALPLYILFRVV
 PQRLPGGDQEIPICTLDPNRIGEISWDVFFETLNFLVPLVIVISYSKILQITKSRKR
 LTLSLAYSESHQIRVSQQDYRLFRTLFLLMVSFFIMWSPIIITILLILIQNFRQDLVIWP
 SLFFWVVAFTFANSALNPILYNMSLFRNEWKIFCCFPPEKGAIFTDTSVRRNDLSVIS
 S*

FIG. 10.

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Prosite Pattern Matches for 14273m,

>PS00001/PDOC00001;ASN_GLYCOSYLATION N-glycosylation site.

Query: 21 NRTH 24
Query: 322 NRTH 325

>PS00002/PDOC00002/GLYCOSAMINOGLYCAN Glycosaminoglycan attachment site.

RU Additional rules:
RU There must be at least two acidic amino acids (Glu or Asp) from -2 to
 -4 relative to the serine.

Query: 148 SGPG 151

>PS00004/PDOC00004/CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation

Query: 239 KRLT 242

>PS00005/PDOC00005/PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.

Query: 237 SRK 239
Query: 350 SVR 352

>PS00006/PDOC00006/CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.

Query: 40 SVVE 43
Query: 256 SQQD 259

>PS00008/PDOC00008/MYRISTYL N-myristoylation site.

Query: 57 GNVCAL 62
Query: 72 GASASL 77
Query: 343 GAIFTD 348

>PS00009/PDOC00009/AMIDATION Amidation site.

Query: 150 PGRR 153

FIG. 11.

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Transmembrane Segments Predicted by MEMSAT

Start	End	Orient	Score
46	66	out->ins	5.1
77	98	ins->out	3.3
113	134	out->ins	3.8
156	177	ins->out	4.5
209	227	out->ins	2.4
266	289	ins->out	6.5
297	321	out->ins	3.2

>14273m,

MSPECAQTTGPGPSHTLDQVNRTHFPFFSDVKGDHRLVLSVVETTVLGLIFVVSLLGNVC
 ALVLVARRRRRGASASLVNLFCADLLFTSAIPLVLVVRWTEAWLLGPVVCHLLFYVMTM
 SGSVTILTAAVSLERMVCIVRLRRGLSGPGRRTQAALLAFIWGYSALAALPLYILFRVV
 PQLPGGDQEIPICITLDWPNRIGESISWDVFFETLNLFLVPLVIVISYSKILQITKASRK
 RLTLSLAYSESHQIRVSQQDYRLFRTLFLLMVSFFIMWSPIIITILLILIQNFRQDLVIWP
 SLFFWVVAFTFANSALNPILYMMSLFRNEWKIFCCFFFPEKGAIIFTDTSVRRNDLSVIS
 S

Transmembrane Segments for Presumed Mature Peptide

Start	End	Orient	Score
16	37	ins->out	3.3
52	73	out->ins	3.8
95	116	ins->out	4.5
148	166	out->ins	2.4
205	228	ins->out	6.5
236	260	out->ins	3.2

>14273m, _mature

LVLVARRRRRGASASLVNLFCADLLFTSAIPLVLVVRWTEAWLLGPVVCHLLFYVMGMS
 GSVTILTAAVSLERMVCIVRLRRGLSGPGRRTQAIIAFIWGYSALAALPLYILFRVVP
 QRLPGGDQEIPICITLDWPNRIGESISWCVFFETLNLFLVPLVIVISYSKILQITKASRKRL
 TLSLAYSESKQIRVSQQDYRLFRTLFLLMVSFFTMWSPIIITILLILIQNFRQDLVIWPS
 LFFWVVAFTFANSALNPILYNMSLFRNEWKIFCCFFFPEKGAIIFTDTSVRRNDLSVISS

FIG. 12.